

Amendments to the Drawings:

Please add the following new drawings, Figures 11, 12, 13, 14, 15, 16, 17, 18 and 19, after Figure 10. The attached new sheets of drawings includes Figures 11, 12, 13, 14, 15, 16, 17, 18 and 19 to be added.

Attachment: New Sheets

(3) Sequence Description: Figure 11

1 ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC
5 MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro 16

49 ACTCGACTTCTTTGGAATATCTTGAAGAAAAATATGAAGAGGCATTTG
ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu 32

10 97 TATGAGCGCGATGAAGGTGATAAATGGCGAACAAAAAGTTGAATTG
TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu 48

15 145 GGTTGGAGTTCCAATCTTCCTTATTATATTGATGGTGTGATGTTAAA
GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys 64

193 TTAACACAGTCTATGCCATCACGTTATATAGCTGACAAGCACAAC
LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn 80

20 241 ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTCAATGCTTGAA
MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu 96

289 GGAGCGGTTTGGATATTAGATAACGGTGTTCGAGAATTGCATATAGT
GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer 112

25 337 AAAGACTTTGAAACTCTCAAAGTTGATTTCTTAGCAAGCTACCTGAA
LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu 128

30 385 ATGCTGAAAATGTCGAAGATCGTTATGTCATAAACATATTAAAT
MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn 144

433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT
GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp 160

35 481 GTTGTAAATGGACCAATGTGCCTGGATGCGTCCCCAAAATTA
ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu 176

529 GTTTGTTTAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC
 ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr 192

5 577 TTGAAATCCAGCAAGTATATAGCATGGCCTTGCAGGGCTGGCAAGCC
 LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla 208

10 625 ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCGCGT
 ThrPheGlyGlyGlyAspHisProProLysSerAspLeuValProArg 224

15 673 GGATCCATGAGCACGATTCCAAACCTCAAAGAAAACCAAACGTAAC
 GlySerMetSerThrIleProLysProGlnArgLysThrLysArgAsn 240

20 721 ACCAACCGTCGCCACAGGAATTACATCGTACTGACTGA
 ThrAsnArgArgProGlnGluPheIleValThrAspEnd 252

25 (4) Sequence Description: Figure 12

1 1 ATGTCCCCCTATACTAGGTTATTGGAAAATTAAAGGGCCTTGTGCAACCC
 MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro 16

20 49 ACTCGACTTCTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTG
 ThrArgLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu 32

25 97 TATGAGCGCGATGAAGGTGATAAATGGCGAACAAAAAGTTGAATTG
 TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu 48

30 145 GGTTTGGAGTTCCCAATCTCCTTATTATATTGATGGTGATGTTAAA
 GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys 64

35 193 TTAACACAGTCTATGCCATCATACGTTATATAGCTGACAAGCACAAC
 LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn 80

40 241 ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTCAATGCTTGAA
 MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu 96

45 289 GGAGCGGTTTGGATATTAGATAACGGTGTTCGAGAATTGCATATAGT
 GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer 112

337 AAAGACTTTGAAACTCTCAAAGTTGATTTCTTAGCAAGCTACCTGAA
LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu 128

5 385 ATGCTGAAAATGTTCGAACGATCGTTATGTCATAAACATATTAAAT
MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn 144

433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTGAT
GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp 160

10 481 GTTGTAAACATGGACCCAATGTGCCTGGATGCGTTCCAAAATTAA
ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu 176

529 GTTGTTTAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC
15 ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr 192

577 TTGAAATCCAGCAAGTATATAGCATGGCCTTGCAAGGGCTGGCAAGCC
LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla 208

20 625 ACGTTGGTGGTGGCGACCATCCTCCAAATCGGATCTGGTTCCGCGT
ThrPheGlyGlyAspHisProProLysSerAspLeuValProArg 224

673 GGATCCGACGTCAAGTTCCCGGGTGGCGGTCAAGATCGTTGGTGGAGTT
25 GlySerAspValLysPheProGlyGlyGlnIleValGlyGlyVal 240

721 TACTTGTGCCGCGCAGGGAATTCATCGTGACTGACTGA
TyrLeuLeuProArgArgGluPheIleValThrAspEnd 252

5

(6) Sequence Description: Figure 13

1 ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC
MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro 16

10 49 ACTCGACTTCTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTG
ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu 32

15 97 TATGAGCGCGATGAAGGTGATAAAATGGCGAAACAAAAAGTTGAATTG
TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu 48

20 145 GGTGGAGTTCCCAATCTCCTTATTATATTGATGGTGATGTTAAA
GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys 64

25 193 TTAACACAGTCTATGCCATCACGTTATAGCTGACAAGCACAAAC
LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn 80

30 241 ATGTTGGGTGGTGTCCAAAAGAGCGTGCAGAGATTCAATGCTTGAA
MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu 96

35 289 GGAGCGGTTTGGATATTAGATAACGGTGTTCGAGAATTGCATATAGT
GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer 112

30 337 AAAGACTTGAAACTCTCAAAGTTGATTTCTAGCAAGCTACCTGAA
LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu 128

385 ATGCTGAAAATGTCGAAGATCGTTATGTCATAAACATATTTAAAT
MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn 144

35 433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTGAT
GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp 160

481	GTGTTTATACATGGACCAATGTGCCTGGATGCCTCCAAAATTA ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu	176
5	529 GTTTGTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr	192
	577 TTGAAATCCAGCAAGTATATAGCATGGCCTTGCAGGGCTGGCAAGCC LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla	208
10	625 ACGTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCCGT ThrPheGlyGlyAspHisProProLysSerAspLeuValProArg	224
15	673 GGATCCAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAACACC GlySerSerThrIleProLysProGlnArgLysThrLysArgAsnThr	240
	721 AACCGTCGCCACAGGACGTCAAGTTCCGGGTGGCGGTCAAGATCGTT AsnArgArgProGlnAspValLysPheProGlyGlyGlnIleVal	256
20	769 GGTGGAGTTACTTGTTGCCGCGCAGGAATTCACTCGTACTGACTGA GlyGlyValTyrLeuLeuProArgArgGluPheIleValThrAspEnd	271

(7) Sequence Description: Figure 14

5'-GATCCATGAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGC
CCACAGG-3'

(8) Sequence Description: Figure 15

5'-AATTCCCTGTGGCGACGGTTGGTGTACGTTGGTTTCTTGAGGTTGGGAATCGT
GCTCATG-3'

(9) Sequence Description: Figure 16

5'-GATCCGACGTCAAGTTCCGGGTGGCGGTCAAGATCGTTGGTGGAGTTACTTGTTGCCG
CGCAGGG-3'

(10) Sequence Description: Figure 17

5'-AATTCCCTGCGCGGACAACAAGTAAACTCCACCAACGATCTGACCGCCACCCGGGAACCT
GACGTCG-3'

- (13) Sequence Description: Figure 18
5'-GAATTCTTACCTGCGCGGCAACAAGTAAACTC-3'
(14) Sequence Description: Figure 19
5'-GCTGGATCCAGCACGATTCCAAACCTCAAAG-3'